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MLVA ANALYSIS OF *SALMONELLA*

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STATENS SERUM INSTITUT

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Background

Salmonella enterica consists of 1500 serovars and causes salmonellosis in humans and animals. Multiple-Locus Variable-number of tandem repeats Analysis (MLVA) has successfully been used for epidemiological investigations of *S.* Enteritidis and *S.* Typhimurium. A range of serovars causes salmonellosis, but since most MLVA protocols are serovar specific, no efficient method can genotype several serovars simultaneously. In this study we developed a general 5-locus MLVA assay for typing of several Salmonella serovars.

Method

66 unique VNTRs were investigated and the polymorphisms of seven promising VNTRs were evaluated with a panel 163 diverse isolates/14 serovars. Five VNTRs were selected for MLVA analysis. The discriminatory power was evaluated within the 14 serovars and compared with that of PFGE. Six pairs (six serovars) of outbreak-related strains were included.

Results

MLVA exhibited 100% *in vitro* stability and contained only true repeats. When analyzing 163 isolates MLVA obtained 79 genotypes (DI of 0.98) and PFGE revealed 86 genotypes (DI of 0.99). Each serotype displayed 2-8 different MLVA-profiles and MLVA identified the isolates from potential outbreaks.

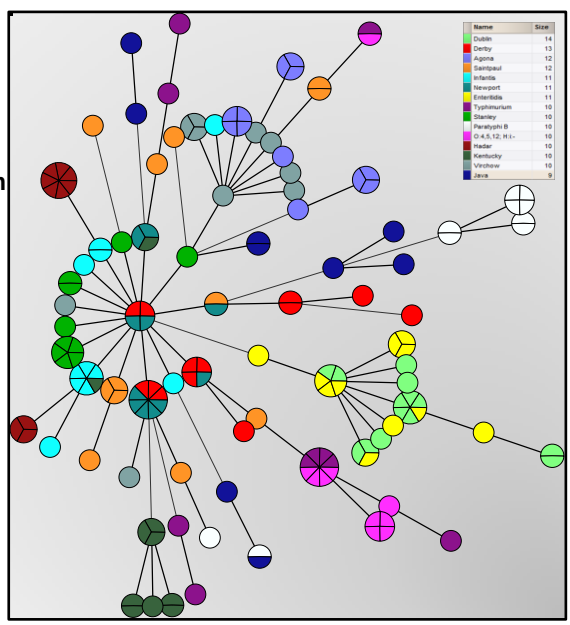
Conclusion

This MLVA

- provides a good discrimination within all serovars, egual to that of PFGE,
- is fast, cheap and provides straightforward genotype identification,
- can be used as a single method for routine subtyping of isolates for surveillance and outbreak investigations, and
- enables rapid cross-country surveillance of multiple *Salmonella* serovars, which may improve the effectiveness of global *Salmonella* surveillance.

	No. of isolates			Alleles in VNTRs by 14 serotypes				
Serovar	Total	PFGE profiles	MLVA profiles	STTR3	STTR5	STTR9	SG2	Sty19
Enteritidis	11	5	7	009ed, 10ed	9-12	1	2-4	1
Typhimurium	10	8	8	211, 212, 409	8, 11-14, 16-17	2-3	2	1
Infantis	11	8	6	112, 114	18, 20-24	1	2	1-2
4,[5],12:i:-	10	4	4	211	11-14	1	2	1
Virchow	10	9	8	114	6-8, 10-11, 13-15	1	2	1
Newport	11	5	5	111, 112	10-12, 17	1	2	1
Stanley	10	7	5	112, 113	4-8, 10	1	2	1
Derby	13	6	9	111, 112	9-12	1	2-4	NA, 1
Kentucky	10	8	6	112, 510	11-13, 17, 20	1	1-2	NA, 1
Agona	12	5	5	113, 114	6-7	1	3-5	1
Saintpaul	12	6	9	011, 111, 113, 211	7, 9-13, 17, 19	1	2	NA, 1, 8
Hadar	10	2	2	110	20-21	1	2	1
Paratyphi B var. Java	9	7	8	110, 111, 113	7, 9-10, 17-18, 24	0-1	2-3	1, 4-5, 9
Paratyphi B	10	5	5	011, 111	9, 11-12	0-1	2	1-2, 6-7
Dublin	14	2	7	010ed	2, 10-13, 15-16	1	3-4	1

Isolates and VNTR's used in this study. Allelic diversity for 5 VNTRs in a panel of 163 diverse isolates.



MST constructed using MLVA profiles from isolates recovered from humans. Serotype is marked with color. MLVA identified 79 genotypes and provided good discrimination within all 14 serotypes.